The figures have been amended to insert SEQ ID NO: 1 after the word "Fig. 1a" on pages 1/23 to 3/23; SEQ ID NOS 15, 4, 5, 6 and 16 for the sequences denoted by "Csk", "Yes", "Ctrl", "B-raf" and "Ilk" respectively in Figure 1b on pages 4/23 and 5/23, and SEQ ID NO. 17, 18, 19, 20, 21 for the sequences denoted by "Ankyrin Consensus", ANK1, ANK2, ANK3 and ANK4 respectively in Figure 1c on page 6/23.

No new matter is added.

Attached hereto is a marked-up version of the changes made to the present application by the present amendment. The attached is captioned "Version with Markings to Show Changes Made".

Applicants respectfully request consideration of the application in view of the amendments and remarks made herein.

Certification Regarding Sequence Listing

I hereby certify that the enclosed Sequence Listing is being submitted under 37 CFR §§ 1.821(c) and (e) in paper and computer readable form (Compact Disk labeled 'CRF').

As required by 37 CFR 1.821(f), I hereby state that the content of the paper and computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821(c) and (e) are the same. The Computer Readable Format (CRF), being submitted under 37 CFR §§ 1.52(e) and 1.824, is formatted on IBM-PC, the operating system compatibility is MS-Windows and the file listing is:

Seqlist.txt 37.5 KB created October 29, 2002.

I hereby certify that the enclosed submission includes no new matter. The Sequence Listing was prepared with the software FASTSEQ, and conforms to the Patent Office guidelines. Applicant respectfully submits that the subject application is in adherence to 37 CFR §§ 1.821-1.825.

Respectfully submitted,

Dated: October 30, 2002

By: Pamela Sherwood

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"Version with markings to Show Changes Made"

In the specification:

On page 28, please amend the paragraph starting on line 14 to read:

FIG. 1 shows yeast two-hybrid cloning, characterization, and expression of ILK. The full length ILK cDNA, Plac5, was isolated from a human placental library using the BIT-9 insert. Plac5 contains a 1509 bp open reading frame, with a presumptive initiator Met at nt 157, and an AAUAAA (SEQ ID NO: 13) signal 11 bp upstream of the polyadenylation site. *In vitro* transcription and translation of Plac5 in rabbit reticulocyte lysates yielded a protein of apparent Mr of 59 kDa. (b) A search of the PIR protein database indicated homology with protein kinase subdomains I to XI, as identified by Hanks et al. We note sequence variations in the ILK subdomains I, VIb, and VII, relative to catalytic domains of known protein kinases. Subdomain I (residues 199-213), does not have the typical GXGXXG (SEQ ID NO: 14) motif, although this region in ILK is Gly-rich. In subdomain Vlb, Asp328 of ILK may compensate for the lack of the otherwise conserved Asp319. In subdomain VII, the DFG triplet is absent in ILK. The integrin binding site maps to amino acid residues 293-451 (BIT-9). The ILK kinase domain is most highly related to the CTR1 kinase of Arabidopsis thaliana (30% identity, P<10). The CTR1, B-raf, Yes and Csk kinase domains are aligned with Plac5. (c) Amino acid residues 33-164 comprise four contiguous ankyrin repeats, as defined by Lux et. al. (d) BIT-9 was used to probe a blot of poly A+ selected RNA (MTN I, Clontech) from various human tissues. (e) Whole cell lysates of mouse, rat and human cell lines (10 μg/lane) were analyzed by Western blotting with the affinity-purified 92-2 antibody (see description of methods in Example 3). The ILK sequence data are available from GenBank under accession number U40282.